



1

SEQUENCE LISTING

<110> HUGANIR, RICHARD L.  
KIM, GJEEHAE

<120> SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF

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<140> 09/294,298

<141> 1999-04-19

<150> 60/082,690

<151> 1998-04-22

<150> 60/082,717

<151> 1998-04-23

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<170> PatentIn Ver. 2.1

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<223> Description of Unknown Organism: mammalian  
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 740 745 750  
 Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met  
 755 760 765  
 Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro  
 770 775 780  
 Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg  
 785 790 795 800  
 Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu  
 805 810 815  
 Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln  
 820 825 830

Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu  
 835 840 845  
 Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala  
 850 855 860  
 Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser  
 865 870 875 880  
 Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val  
 885 890 895  
 Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe  
 900 905 910  
 Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala  
 915 920 925  
 Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His  
 930 935 940  
 His His His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr  
 945 950 955 960  
 Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly  
 965 970 975  
 Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser  
 980 985 990  
 Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser  
 995 1000 1005  
 Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile  
 1010 1015 1020  
 Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly  
 1025 1030 1035 1040  
 Gly Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly  
 1045 1050 1055  
 Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser  
 1060 1065 1070  
 Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg  
 1075 1080 1085  
 Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly  
 1090 1095 1100  
 Gly Ser Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys  
 1105 1110 1115 1120  
 Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser  
 1125 1130 1135

Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp  
 1140 1145 1150  
 Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr  
 1155 1160 1165  
 Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu  
 1170 1175 1180  
 Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys  
 1185 1190 1195 1200  
 Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser  
 1205 1210 1215  
 Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg  
 1220 1225 1230  
 Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile  
 1235 1240 1245  
 Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala  
 1250 1255 1260  
 Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln  
 1265 1270 1275 1280  
 Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro  
 1285 1290 1295  
 His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly  
 1300 1305 1310  
 Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser  
 1315 1320 1325  
 Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro  
 1330 1335 1340  
 Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser  
 1345 1350 1355 1360  
 Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro  
 1365 1370 1375  
 Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser  
 1380 1385 1390  
 Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His  
 1395 1400 1405  
 Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro  
 1410 1415 1420

&lt;210&gt; 3

&lt;211&gt; 4134

&lt;212&gt; DNA

&lt;213&gt; Unknown Organism

&lt;220&gt;

<223> Description of Unknown Organism: mammalian  
SYNGAP-B

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(3741)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3745)..(4134)

&lt;400&gt; 3

taa	ggc	ccc	cca	ccc	cga	ccc	cgt	cag	ggg	gct	ccg	gtt	cag	gtt	cct	48
	Gly	Pro	Pro	Pro	Arg	Pro	Arg	Gln	Gly	Ala	Pro	Val	Gln	Val	Pro	
	1				5				10						15	

tgc	ccc	ctc	ctt	ccc	acc	gcc	agc	ctc	tcc	gcc	gcc	gct	gct	ctt	cct	96
Cys	Pro	Leu	Leu	Pro	Thr	Ala	Ser	Leu	Ser	Ala	Ala	Ala	Ala	Leu	Pro	
				20					25					30		

gct	gct	ttc	cgg	ggg	aat	acc	act	tgg	gtc	gct	cga	gga	gga	aga	gtg	144
Ala	Ala	Phe	Arg	Gly	Asn	Thr	Thr	Trp	Val	Ala	Arg	Gly	Gly	Arg	Val	
			35					40					45			

tcc	ccg	ggg	ggg	aaa	cag	tac	agc	atg	gaa	gcc	gcc	ccc	gct	gcg	ccc	192
Ser	Pro	Gly	Gly	Lys	Gln	Tyr	Ser	Met	Glu	Ala	Ala	Pro	Ala	Ala	Pro	
		50					55					60				

ttc	cgg	ccc	tcg	caa	ggc	ttc	ctg	agc	cgg	agg	cta	aaa	agc	tcc	atc	240
Phe	Arg	Pro	Ser	Gln	Gly	Phe	Leu	Ser	Arg	Arg	Leu	Lys	Ser	Ser	Ile	
	65					70					75					

aaa	cgt	aca	aag	tca	caa	ccc	aaa	ctt	gac	cgg	acc	agc	agc	ttt	cga	288
Lys	Arg	Thr	Lys	Ser	Gln	Pro	Lys	Leu	Asp	Arg	Thr	Ser	Ser	Phe	Arg	
	80				85				90						95	

cag	atc	ctg	cct	cgc	ttc	cga	agt	gct	gac	cat	gac	cgg	gcc	cgg	ctg	336
Gln	Ile	Leu	Pro	Arg	Phe	Arg	Ser	Ala	Asp	His	Asp	Arg	Ala	Arg	Leu	
				100					105					110		

atg	cag	agc	ttc	aag	gag	tct	cac	tcc	cat	gag	tcc	ctg	ctg	agt	ccc	384
Met	Gln	Ser	Phe	Lys	Glu	Ser	His	Ser	His	Glu	Ser	Leu	Leu	Ser	Pro	
			115					120					125			

agc	agt	gct	gct	gag	gcc	ctg	gag	ctc	aac	ctg	gat	gaa	gac	tcc	att	432
Ser	Ser	Ala	Ala	Glu	Ala	Leu	Glu	Leu	Asn	Leu	Asp	Glu	Asp	Ser	Ile	
		130				135					140					

atc	aag	cca	gta	cac	agc	tcc	atc	ctg	ggc	cag	gag	ttc	tgc	ttt	gag	480
Ile	Lys	Pro	Val	His	Ser	Ser	Ile	Leu	Gly	Gln	Glu	Phe	Cys	Phe	Glu	
	145					150				155						



gta aca aca tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala 160 165 170 175	528
gaa agg gac aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn 180 185 190	576
aag gac aac agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile 195 200 205	624
gaa gct cga gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys 210 215 220	672
ctg gac gac atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala 225 230 235	720
tca gga gac act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu 240 245 250 255	768
cct gct gtc cgg gcg ctg cgg ctg cat ctg tac cgt gac tcg gac aaa Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys 260 265 270	816
aag cgg aag aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca Lys Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro 275 280 285	864
gtg gcc acc ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val 290 295 300	912
acc ctg cca aca gga agt ggg ggc tct ggg ggt atg ggc tcg ggg gga Thr Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly 305 310 315	960
gga ggg ggg tca ggg ggc ggc tca ggg ggc aaa ggg aaa gga ggc tgt Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys 320 325 330 335	1008
cct gct gtg cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc Pro Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro 340 345 350	1056
atg gag cta tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc Met Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg 355 360 365	1104
atg ctg tgt gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag Met Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu 370 375 380	1152

gag gtc gct agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc Glu Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala 385 390 395	1200
aag gac ttc ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met 400 405 410 415	1248
gag cgg gaa cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala 420 425 430	1296
ata gaa gag tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala 435 440 445	1344
att ggg gag ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu 450 455 460	1392
gta gac ccc atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala 465 470 475	1440
aac ctg cgg atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser 480 485 490 495	1488
cat tgc gtg ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg 500 505 510	1536
ctg cgc tgt gca gag cgg ggc cgg gag gac att gct gac agg ctg atc Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile 515 520 525	1584
agc gcc tcg ctc ttc ctg cgc ttc ctc tgc ccg gcc atc atg tcg ccc Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro 530 535 540	1632
agt ctg ttt gga ctg atg cag gag tac cca gat gag cag acc tca cga Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg 545 550 555	1680
acc ctc acc ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser 560 565 570 575	1728
aag ttt acc tca aag gag gac ttc ctg ggc ttc atg aac gag ttt ctg Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu 580 585 590	1776
gag ctg gag tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn 595 600 605	1824

ctg gac aca ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg Leu Asp Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu 610 615 620	1872
ggc cgc gag ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc Gly Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro 625 630 635	1920
cag ctc agc aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu 640 645 650 655	1968
ctc agc gac atc agc aca gcc ctg agg aac cct aac atc caa agg cag Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln 660 665 670	2016
ccg agc cgc cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg 675 680 685	2064
ggg ccg tca gcc gag atg cag ggc tac atg atg cgg gac ctc aac agc Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser 690 695 700	2112
tcc atc gac ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met 705 710 715	2160
gac atg gct cgc ctc ccc tcc cca acc aag gag aaa ccc ccg ccg ccc Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro 720 725 730 735	2208
cct ccc ggt ggg ggt aaa gac ctg ttc tat gtg agc cgg cca cca ctg Pro Pro Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu 740 745 750	2256
gcc cgg tcc tcc cca gca tac tgc acg agc agc tcg gac atc aca gag Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu 755 760 765	2304
ccg gag cag aag atg ctg agt gtc aac aag agt gtg tcc atg ctg gac Pro Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp 770 775 780	2352
ctg cag ggc gac ggg cct ggg ggc cgc ctt aac agc agt agt gtt tcc Leu Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser 785 790 795	2400
aac ctg gca gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu 800 805 810 815	2448
aca gca gcc ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln 820 825 830	2496

ggg agt ggc tct tcc atc aca gca gcc ggc atg cgc ctc agc cag atg Gly Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met 835 840 845	2544
ggt gtc act acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu 850 855 860	2592
tcc ttc cag aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro 865 870 875	2640
cca gca ggc cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat Pro Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His 880 885 890 895	2688
cac cac cac cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg His His His His His His His His His Arg Gly Gly Glu Pro Pro Gly 900 905 910	2736
gac act ttt gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct Asp Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser 915 920 925	2784
aca ggg gtc cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc Thr Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser 930 935 940	2832
tac agt gat gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag Tyr Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln 945 950 955	2880
ctc tca ctt cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc Leu Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile 960 965 970 975	2928
acc atc ggt ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt Thr Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser 980 985 990	2976
ggt ggg ggc agt ggt ggg ggc ggt ggg ggc cag cca cct ccc ttg cag Gly Gly Gly Ser Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln 995 1000 1005	3024
agg ggc aaa tct cag cag ttg aca gtg agt gct gcc cag aaa ccc cgg Arg Gly Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg 1010 1015 1020	3072
ccg tcc agc ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct Pro Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro 1025 1030 1035	3120
gcc cgt cca cgg caa cag agc ctc agc aaa gag ggc agc att ggg ggc Ala Arg Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly 1040 1045 1050 1055	3168

agc ggg ggc agc ggt ggc gga ggg ggt ggg ggg ctc aag ccc tcc atc Ser Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile 1060 1065 1070	3216
acc aag cag cat tcc cag act cca tcc acg ctg aac ccc acg atg ccg Thr Lys Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro 1075 1080 1085	3264
gcc tcg gag cgg act gta gcc tgg gtg tcc aat atg cct cac ctg tcc Ala Ser Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser 1090 1095 1100	3312
gct gac atc gag agt gca cac att gag cgg gaa gag tac aag ctg aag Ala Asp Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys 1105 1110 1115	3360
gag tac tcg aag tcc atg gac gag agc cga ctg gac agg gtg aag gag Glu Tyr Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu 1120 1125 1130 1135	3408
tac gag gag gag atc cac tca ctg aag gaa agg cta cac atg tcc aac Tyr Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn 1140 1145 1150	3456
cgg aag ctg gaa gag tac gag cgg agg ctg ctg tcc cag gaa gag cag Arg Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln 1155 1160 1165	3504
acc agc aag atc ctg atg cag tac caa gcc cgc ctg gag cag agc gag Thr Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu 1170 1175 1180	3552
aag cgc ttg agg cag cag cag gtg gag aag gac tcc cag atc aag agc Lys Arg Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser 1185 1190 1195	3600
atc att ggc agg ctg atg ctg gtg gag gag gag ctg cgc cgg gac cac Ile Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His 1200 1205 1210 1215	3648
ccc gcc atg gct gag ccg ctg cct gaa ccc aag aag agg ctg ctc gac Pro Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp 1220 1225 1230	3696
gct cag aga ggc agc ttc ccc cct tgg gtc caa caa acc cgc gtg Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val 1235 1240 1245	3741
tga cgc tgg ccc cac ctt gga acg gcc tgg ccc ccc cag ccc cac ccc Arg Trp Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro 1250 1255 1260	3789
ccc cac ccc ggc tgc aga tca cag aga acg gcg agt tcc gga aca ccg Pro His Pro Gly Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro 1265 1270 1275	3837



cag acc act agc cca ccc agc atc aca gac ctc ctt ccc tgt gca ccc 3885  
 Gln Thr Thr Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro  
 1280 1285 1290

tac ccc ggc cca ccc agc gtc aca gac ctc ctt ccc agt gca ccc gac 3933  
 Tyr Pro Gly Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp  
 1295 1300 1305

cct gga aca tca cca acc acc agg act gga cgt cac caa ggg aca gcg 3981  
 Pro Gly Thr Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala  
 1310 1315 1320 1325

gga ttg tct ccc tta acg cct cct tgg ggc acc cat ctg tca acc cca 4029  
 Gly Leu Ser Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro  
 1330 1335 1340

ctg ctc cat tcc agg agg gag agt ggg acc ctc agc tgc cct ctc acc 4077  
 Leu Leu His Ser Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr  
 1345 1350 1355

cca gga cac cac cta ccc cac aca gac ccc ttc act ctg ggg tgc tat 4125  
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 1360 1365 1370

ccc cat cct 4134  
 Pro His Pro  
 1375

&lt;210&gt; 4

&lt;211&gt; 1376

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

 <223> Description of Unknown Organism: mammalian  
 SYNGAP-B

&lt;400&gt; 4

Gly Pro Pro Pro Arg Pro Arg Gln Gly Ala Pro Val Gln Val Pro Cys  
 1 5 10 15

Pro Leu Leu Pro Thr Ala Ser Leu Ser Ala Ala Ala Ala Leu Pro Ala  
 20 25 30

Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Gly Arg Val Ser  
 35 40 45

Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe  
 50 55 60

Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys  
 65 70 75 80

Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln  
 85 90 95

Ile	Leu	Pro	Arg	Phe	Arg	Ser	Ala	Asp	His	Asp	Arg	Ala	Arg	Leu	Met
			100					105					110		
Gln	Ser	Phe	Lys	Glu	Ser	His	Ser	His	Glu	Ser	Leu	Leu	Ser	Pro	Ser
		115					120					125			
Ser	Ala	Ala	Glu	Ala	Leu	Glu	Leu	Asn	Leu	Asp	Glu	Asp	Ser	Ile	Ile
	130					135					140				
Lys	Pro	Val	His	Ser	Ser	Ile	Leu	Gly	Gln	Glu	Phe	Cys	Phe	Glu	Val
145					150					155					160
Thr	Thr	Ser	Ser	Gly	Thr	Lys	Cys	Phe	Ala	Cys	Arg	Ser	Ala	Ala	Glu
				165					170					175	
Arg	Asp	Lys	Trp	Ile	Glu	Asn	Leu	Gln	Arg	Ala	Val	Lys	Pro	Asn	Lys
			180					185					190		
Asp	Asn	Ser	Arg	Arg	Val	Asp	Asn	Val	Leu	Lys	Leu	Trp	Ile	Ile	Glu
		195					200					205			
Ala	Arg	Glu	Leu	Pro	Pro	Lys	Lys	Arg	Tyr	Tyr	Cys	Glu	Leu	Cys	Leu
	210					215					220				
Asp	Asp	Met	Leu	Tyr	Ala	Arg	Thr	Thr	Ser	Lys	Pro	Arg	Ser	Ala	Ser
225					230					235					240
Gly	Asp	Thr	Val	Phe	Trp	Gly	Glu	His	Phe	Glu	Phe	Asn	Asn	Leu	Pro
				245					250					255	
Ala	Val	Arg	Ala	Leu	Arg	Leu	His	Leu	Tyr	Arg	Asp	Ser	Asp	Lys	Lys
			260					265					270		
Arg	Lys	Lys	Asp	Lys	Ala	Gly	Tyr	Val	Gly	Leu	Val	Thr	Val	Pro	Val
		275					280					285			
Ala	Thr	Leu	Ala	Gly	Arg	His	Phe	Thr	Glu	Gln	Trp	Tyr	Pro	Val	Thr
	290					295					300				
Leu	Pro	Thr	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Met	Gly	Ser	Gly	Gly	Gly
305					310					315					320
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Lys	Gly	Lys	Gly	Gly	Cys	Pro
				325					330					335	
Ala	Val	Arg	Leu	Lys	Ala	Arg	Tyr	Gln	Thr	Met	Ser	Ile	Leu	Pro	Met
			340					345					350		
Glu	Leu	Tyr	Lys	Glu	Phe	Ala	Glu	Tyr	Val	Thr	Asn	His	Tyr	Arg	Met
		355					360					365			
Leu	Cys	Ala	Val	Leu	Glu	Pro	Ala	Leu	Asn	Val	Lys	Gly	Lys	Glu	Glu
	370					375					380				
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Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro		
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Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr		
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Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His  
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 Gln Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr  
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Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn	
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Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val	
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Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys	
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Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala	
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Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu	
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Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro	
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Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly	
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&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

<223> Description of Unknown Organism: mammalian  
 SYNGAP-C

&lt;400&gt; 6

Gly Glu Thr Glu Leu Pro Gln Ala Pro His Phe Pro Phe Ala Pro Gln  
   1                  5                  10                  15

Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr Lys  
                   20                  25                  30

Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu Pro  
                   35                  40                  45

Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser Phe  
                   50                  55                  60

Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala Ala  
   65                  70                  75                  80

Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro Val  
                   85                  90                  95

His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr Ser  
                   100                  105                  110

Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp Lys  
                   115                  120                  125

Trp	Ile	Glu	Asn	Leu	Gln	Arg	Ala	Val	Lys	Pro	Asn	Lys	Asp	Asn	Ser
	130					135					140				
Arg	Arg	Val	Asp	Asn	Val	Leu	Lys	Leu	Trp	Ile	Ile	Glu	Ala	Arg	Glu
145					150					155					160
Leu	Pro	Pro	Lys	Lys	Arg	Tyr	Tyr	Cys	Glu	Leu	Cys	Leu	Asp	Asp	Met
				165					170					175	
Leu	Tyr	Ala	Arg	Thr	Thr	Ser	Lys	Pro	Arg	Ser	Ala	Ser	Gly	Asp	Thr
			180					185					190		
Val	Phe	Trp	Gly	Glu	His	Phe	Glu	Phe	Asn	Asn	Leu	Pro	Ala	Val	Arg
		195					200					205			
Ala	Leu	Arg	Leu	His	Leu	Tyr	Arg	Asp	Ser	Asp	Lys	Lys	Arg	Lys	Lys
	210					215					220				
Asp	Lys	Ala	Gly	Tyr	Val	Gly	Leu	Val	Thr	Val	Pro	Val	Ala	Thr	Leu
225					230					235					240
Ala	Gly	Arg	His	Phe	Thr	Glu	Gln	Trp	Tyr	Pro	Val	Thr	Leu	Pro	Thr
				245					250					255	
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Met	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Ser
			260				265						270		
Gly	Gly	Gly	Ser	Gly	Gly	Lys	Gly	Lys	Gly	Gly	Cys	Pro	Ala	Val	Arg
		275					280					285			
Leu	Lys	Ala	Arg	Tyr	Gln	Thr	Met	Ser	Ile	Leu	Pro	Met	Glu	Leu	Tyr
	290					295					300				
Lys	Glu	Phe	Ala	Glu	Tyr	Val	Thr	Asn	His	Tyr	Arg	Met	Leu	Cys	Ala
305					310					315					320
Val	Leu	Glu	Pro	Ala	Leu	Asn	Val	Lys	Gly	Lys	Glu	Glu	Val	Ala	Ser
				325					330					335	
Ala	Leu	Val	His	Ile	Leu	Gln	Ser	Thr	Gly	Lys	Ala	Lys	Asp	Phe	Leu
			340					345					350		
Ser	Asp	Met	Ala	Met	Ser	Glu	Val	Asp	Arg	Phe	Met	Glu	Arg	Glu	His
		355					360					365			
Leu	Ile	Phe	Arg	Glu	Asn	Thr	Leu	Ala	Thr	Lys	Ala	Ile	Glu	Glu	Tyr
	370					375					380				
Met	Arg	Leu	Ile	Gly	Gln	Lys	Tyr	Leu	Lys	Asp	Ala	Ile	Gly	Glu	Phe
385					390					395					400
Ile	Arg	Ala	Leu	Tyr	Glu	Ser	Glu	Glu	Asn	Cys	Glu	Val	Asp	Pro	Ile
				405					410					415	
Lys	Cys	Thr	Ala	Ser	Ser	Leu	Ala	Glu	His	Gln	Ala	Asn	Leu	Arg	Met
			420					425					430		

Cys	Cys	Glu	Leu	Ala	Leu	Cys	Lys	Val	Val	Asn	Ser	His	Cys	Val	Phe	435	440	445
Pro	Arg	Glu	Leu	Lys	Glu	Val	Phe	Ala	Ser	Trp	Arg	Leu	Arg	Cys	Ala	450	455	460
Glu	Arg	Gly	Arg	Glu	Asp	Ile	Ala	Asp	Arg	Leu	Ile	Ser	Ala	Ser	Leu	465	470	475
Phe	Leu	Arg	Phe	Leu	Cys	Pro	Ala	Ile	Met	Ser	Pro	Ser	Leu	Phe	Gly	485	490	495
Leu	Met	Gln	Glu	Tyr	Pro	Asp	Glu	Gln	Thr	Ser	Arg	Thr	Leu	Thr	Leu	500	505	510
Ile	Ala	Lys	Val	Ile	Gln	Asn	Leu	Ala	Asn	Phe	Ser	Lys	Phe	Thr	Ser	515	520	525
Lys	Glu	Asp	Phe	Leu	Gly	Phe	Met	Asn	Glu	Phe	Leu	Glu	Leu	Glu	Trp	530	535	540
Gly	Ser	Met	Gln	Gln	Phe	Leu	Tyr	Glu	Ile	Ser	Asn	Leu	Asp	Thr	Leu	545	550	555
Thr	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Tyr	Ile	Asp	Leu	Gly	Arg	Glu	Leu	565	570	575
Ser	Thr	Leu	His	Ala	Leu	Leu	Trp	Glu	Val	Leu	Pro	Gln	Leu	Ser	Lys	580	585	590
Glu	Ala	Leu	Leu	Lys	Leu	Gly	Pro	Leu	Pro	Arg	Leu	Leu	Ser	Asp	Ile	595	600	605
Ser	Thr	Ala	Leu	Arg	Asn	Pro	Asn	Ile	Gln	Arg	Gln	Pro	Ser	Arg	Gln	610	615	620
Ser	Glu	Arg	Ala	Arg	Ser	Gln	Pro	Met	Val	Leu	Arg	Gly	Pro	Ser	Ala	625	630	635
Glu	Met	Gln	Gly	Tyr	Met	Met	Arg	Asp	Leu	Asn	Ser	Ser	Ile	Asp	Leu	645	650	655
Gln	Ser	Phe	Met	Ala	Arg	Gly	Leu	Asn	Ser	Ser	Met	Asp	Met	Ala	Arg	660	665	670
Leu	Pro	Ser	Pro	Thr	Lys	Glu	Lys	Pro	Pro	Pro	Pro	Pro	Pro	Gly	Gly	675	680	685
Gly	Lys	Asp	Leu	Phe	Tyr	Val	Ser	Arg	Pro	Pro	Leu	Ala	Arg	Ser	Ser	690	695	700
Pro	Ala	Tyr	Cys	Thr	Ser	Ser	Ser	Asp	Ile	Thr	Glu	Pro	Glu	Gln	Lys	705	710	715
Met	Leu	Ser	Val	Asn	Lys	Ser	Val	Ser	Met	Leu	Asp	Leu	Gln	Gly	Asp	725	730	735

Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala Ala  
 740 745 750  
 Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala Leu  
 755 760 765  
 Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly Ser  
 770 775 780  
 Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr Thr  
 785 790 795 800  
 Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln Asn  
 805 810 815  
 Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly His  
 820 825 830  
 Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His  
 835 840 845  
 His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe Ala  
 850 855 860  
 Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val Pro  
 865 870 875 880  
 Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp Glu  
 885 890 895  
 Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu Gln  
 900 905 910  
 Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly Pro  
 915 920 925  
 Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly Gly Ser  
 930 935 940  
 Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys Ser  
 945 950 955 960  
 Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser Gly  
 965 970 975  
 Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro Arg  
 980 985 990  
 Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly Ser  
 995 1000 1005  
 Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln His  
 1010 1015 1020  
 Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu Arg  
 1025 1030 1035 1040

Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile Glu  
 1045 1050 1055  
 Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser Lys  
 1060 1065 1070  
 Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu Glu  
 1075 1080 1085  
 Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu Glu  
 1090 1095 1100  
 Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys Ile  
 1105 1110 1115 1120  
 Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu Arg  
 1125 1130 1135  
 Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly Arg  
 1140 1145 1150  
 Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala Met Ala  
 1155 1160 1165  
 Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg Gly  
 1170 1175 1180  
 Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro His Leu  
 1185 1190 1195 1200  
 Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly Cys Arg  
 1205 1210 1215  
 Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser Pro Pro  
 1220 1225 1230  
 Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro Pro Ser  
 1235 1240 1245  
 Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser Pro Thr  
 1250 1255 1260  
 Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro Leu Thr  
 1265 1270 1275 1280  
 Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser Arg Arg  
 1285 1290 1295  
 Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His Leu Pro  
 1300 1305 1310  
 His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro  
 1315 1320 1325

&lt;210&gt; 7

&lt;211&gt; 216



&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

<223> Description of Unknown Organism: mammalian  
SYNGAP-C

&lt;400&gt; 7

Gly	Lys	Ala	Lys	Asp	Phe	Leu	Ser	Asp	Met	Ala	Met	Ser	Glu	Val	Asp	1	5	10	15
Arg	Phe	Met	Glu	Arg	Glu	His	Leu	Ile	Phe	Arg	Glu	Asn	Thr	Leu	Ala	20	25	30	
Thr	Lys	Ala	Ile	Glu	Glu	Tyr	Met	Arg	Leu	Ile	Gly	Gln	Lys	Tyr	Leu	35	40	45	
Lys	Asp	Ala	Ile	Gly	Glu	Phe	Ile	Arg	Ala	Leu	Tyr	Glu	Ser	Glu	Glu	50	55	60	
Asn	Cys	Glu	Val	Asp	Pro	Ile	Lys	Cys	Thr	Ala	Ser	Ser	Leu	Ala	Glu	65	70	75	80
His	Gln	Ala	Asn	Leu	Arg	Met	Cys	Cys	Glu	Leu	Ala	Leu	Cys	Lys	Val	85	90	95	
Val	Asn	Ser	His	Cys	Val	Phe	Pro	Arg	Glu	Leu	Lys	Glu	Val	Phe	Ala	100	105	110	
Ser	Trp	Arg	Leu	Arg	Cys	Ala	Glu	Arg	Gly	Arg	Glu	Asp	Ile	Ala	Asp	115	120	125	
Arg	Leu	Ile	Ser	Ala	Ser	Leu	Phe	Leu	Arg	Phe	Leu	Cys	Pro	Ala	Ile	130	135	140	
Met	Ser	Pro	Ser	Leu	Phe	Gly	Leu	Met	Gln	Glu	Tyr	Pro	Asp	Glu	Gln	145	150	155	160
Thr	Ser	Arg	Thr	Leu	Thr	Leu	Ile	Ala	Lys	Val	Ile	Gln	Asn	Leu	Ala	165	170	175	
Asn	Phe	Ser	Lys	Phe	Thr	Ser	Lys	Glu	Asp	Phe	Leu	Gly	Phe	Met	Asn	180	185	190	
Glu	Phe	Leu	Glu	Leu	Glu	Trp	Gly	Ser	Met	Gln	Gln	Phe	Leu	Tyr	Glu	195	200	205	
Ile	Ser	Asn	Leu	Asp	Thr	Leu	Thr	210	215										

&lt;210&gt; 8

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 8

Lys Leu Glu Ser Leu Leu Leu Cys Thr Leu Asn Asp Arg Glu Ile Ser  
 1 5 10 15  
 Met Glu Asp Glu Ala Thr Thr Leu Phe Arg Ala Thr Thr Leu Ala Ser  
 20 25 30  
 Thr Leu Met Glu Gln Tyr Met Lys Ala Thr Ala Thr Gln Phe Val His  
 35 40 45  
 His Ala Leu Lys Asp Ser Ile Leu Lys Ile Met Glu Val Gln His Lys  
 50 55 60  
 Trp Pro Thr Asn Asn Thr Met Arg Thr Arg Val Val Ser Gly Phe Val  
 65 70 75 80  
 Phe Leu Arg Leu Ile Cys Pro Ala Ile Leu Asn Pro Arg Met Phe Asn  
 85 90 95  
 Ile Ile Ser Asp Ser Pro Ser Pro Ile Ala Ala Arg Thr Leu Thr Leu  
 100 105 110  
 Val Ala Lys Ser Val Gln Asn Leu Ala Asn Ser Lys Gln Ser Cys Glu  
 115 120 125  
 Leu Ser Pro Ser Lys Leu Glu Lys Asn Glu Asp Val Asn Thr Asn Leu  
 130 135 140  
 Ala His Leu Leu Ser Ile Leu Ser Glu Leu Val Glu Lys Ile Phe Met  
 145 150 155 160  
 Ala Ser Glu Ile Leu Pro Pro Thr Leu Arg Tyr Ile Tyr Gly Cys Leu  
 165 170 175  
 Gln Lys Ser Leu Val Glu Phe Gly Ala Lys Glu Pro Tyr Met Glu Gly  
 180 185 190  
 Val Asn Pro Phe Ile Lys Ser Asn Lys His Arg Met Ile Met Phe Leu  
 195 200 205  
 Asp Glu Leu Gly Asn Val Pro Glu Leu Pro  
 210 215

&lt;210&gt; 9

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

His Leu Leu Tyr Gln Leu Leu Trp Asn Met Phe Ser Lys Glu Val Glu  
 1 5 10 15  
 Leu Ala Asp Ser Met Gln Thr Leu Phe Arg Gly Asn Ser Leu Ala Ser  
 20 25 30  
 Lys Ile Met Thr Phe Cys Phe Lys Val Tyr Gly Ala Thr Tyr Leu Gln  
 35 40 45

Lys	Leu	Leu	Asp	Pro	Leu	Leu	Arg	Ile	Val	Ile	Thr	Ser	Ser	Asp	Trp
50						55					60				
Gln	His	Val	Ser	Phe	Glu	Val	Asp	Pro	Thr	Arg	Leu	Glu	Pro	Ser	Glu
65					70					75					80
Ser	Leu	Glu	Glu	Asn	Gln	Arg	Asn	Leu	Leu	Gln	Met	Thr	Glu	Lys	Phe
				85					90					95	
Phe	His	Ala	Ile	Ile	Ser	Ser	Ser	Ser	Glu	Phe	Pro	Pro	Gln	Leu	Arg
			100					105					110		
Ser	Val	Cys	His	Cys	Leu	Tyr	Gln	Val	Val	Ser	Gln	Arg	Phe	Pro	Gln
		115					120					125			
Asn	Ser	Ile	Gly	Ala	Val	Gly	Ser	Ala	Met	Phe	Leu	Arg	Phe	Ile	Asn
	130					135					140				
Pro	Ala	Ile	Val	Ser	Pro	Tyr	Glu	Ala	Gly	Ile	Leu	Asp	Lys	Lys	Pro
145					150					155					160
Pro	Pro	Arg	Ile	Glu	Arg	Gly	Leu	Lys	Leu	Met	Ser	Lys	Ile	Leu	Gln
				165					170					175	
Ser	Ile	Ala	Asn	His	Val	Leu	Phe	Thr	Lys	Glu	Glu	His	Met	Arg	Pro
			180					185					190		
Phe	Asn	Asp	Phe	Val	Lys	Ser	Asn	Phe	Asp	Ala	Ala	Arg	Arg	Phe	Phe
		195					200					205			
Leu	Asp	Ile	Ala	Ser	Asp	Cys	Pro	Thr	Ser	Asp					
	210					215									

```
<210> 10
<211> 82
<212> PRT
<213> Unknown Organism
```

<220>  
<223> Description of Unknown Organism: mammalian  
SYNGAP-A

```

<400> 10
Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala
  1                      5                      10                      15

Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Lys Lys Pro
      20                      25                      30

Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr
      35                      40                      45

Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp
  50                      55                      60

```

Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn  
 65 70 75 80

Ser Arg

<210> 11  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Phe Tyr Lys Asn Ile Val Lys Lys Gly Tyr Leu Leu Lys Lys Gly Lys  
 1 5 10 15  
 Gly Lys Arg Trp Lys Asn Leu Tyr Phe Ile Leu Glu Gly Ser Asp Ala  
 20 25 30  
 Gln Leu Ile Tyr Phe Glu Ser Glu Lys Arg Ala Thr Lys Pro Lys Gly  
 35 40 45  
 Leu Ile Asp Leu Ser Val Cys Ser Val Tyr Val Val His Asp Ser Leu  
 50 55 60  
 Phe Gly Arg Pro Asn Cys Phe Gln Ile Val Val Gln His Phe Ser Glu  
 65 70 75 80  
 Glu His Tyr Ile Phe Tyr Phe Ala Gly Glu Thr Pro Glu Gln Ala Glu  
 85 90 95  
 Asp Trp Met Lys Gly Leu Gln Ala Phe Cys Asn Leu Arg Lys Ser Ser  
 100 105 110

Pro Gly

<210> 12  
 <211> 111  
 <212> PRT  
 <213> Drosophila melanogaster

<400> 12  
 Pro Val Leu Leu Lys Glu Gly Glu Gly Leu Met Thr Lys Tyr Pro Thr  
 1 5 10 15  
 Ser Arg Lys Arg Phe Gly Arg Gln Phe Lys Gln Arg His Phe Arg Leu  
 20 25 30  
 Thr Thr His Ser Leu Ser Tyr Ala Lys Ser Lys Gly Lys Gln Pro Ile  
 35 40 45  
 Cys Asp Ile Pro Leu Gln Glu Ile Ala Ser Val Glu Gln Leu Lys Asp  
 50 55 60  
 Lys Ser Phe Lys Met Gln Asn Cys Phe Lys Ile Val His Asn Asp Arg  
 65 70 75 80

Ser Leu Ile Val Gln Thr Thr Asn Cys Val Glu Glu Arg Glu Trp Phe  
85 90 95

Asp Leu Leu His Lys Ile Cys Leu Met Asn Ser Ile Arg Met Gln  
100 105 110

```
<210> 13
<211> 108
<212> PRT
<213> Homo sapiens
```

```
<400> 13
Met Glu Pro Lys Arg Ile Arg Glu Gly Tyr Leu Val Lys Lys Gly Ser
  1             5             10            15
```

Val Phe Asn Thr Trp Lys Pro Met Trp Val Val Leu Leu Glu Asp Gly  
20 25 30

Ile Glu Phe Tyr Lys Lys Lys Ser Asp Asn Ser Pro Lys Gly Met Ile  
35 40 45

Pro Leu Lys Gly Ser Thr Leu Thr Ser Pro Cys Gln Asp Phe Gly Lys  
50 55 60

Arg Met Phe Val Phe Lys Ile Thr Thr Thr Lys Gln Gln Asp His Phe  
65 70 75 80

Phe Gln Ala Ala Phe Leu Glu Glu Arg Asp Ala Trp Val Arg Asp Ile  
85 90 95

Asn Lys Ala Ile Lys Cys Ile Glu Gly Gly Gln Lys  
100 105

```
<210> 14
<211> 110
<212> PRT
<213> Unknown Organism
```

<220>  
<223> Description of Unknown Organism: mammalian  
SYNGAP-A

```
<400> 14
Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu Leu Pro
  1           5           10          15
```

Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met Leu Tyr  
20 25 30

Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr Val Phe  
35 40 45

Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg Ala Leu  
50 55 60

40

Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys Asp Lys  
65 70 75 80

Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu Ala Gly  
85 90 95

Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr  
100 105 110

<210> 15

<211> 107

<212> PRT

<213> Homo sapiens

<400> 15

Gln Val Ser Ser Leu Val Leu His Ile Glu Glu Ala His Lys Leu Pro  
1 5 10 15

Val Lys His Phe Thr Asn Pro Tyr Cys Asn Ile Tyr Leu Asn Ser Val  
20 25 30

Gln Val Ala Lys Thr His Ala Arg Glu Gly Gln Asn Pro Val Trp Ser  
35 40 45

Glu Glu Phe Val Phe Asp Asp Leu Pro Pro Asp Ile Asn Arg Phe Glu  
50 55 60

Ile Thr Leu Ser Asn Lys Thr Lys Lys Ser Lys Asp Pro Asp Ile Leu  
65 70 75 80

Phe Met Arg Cys Gln Leu Ser Arg Leu Gln Lys Gly His Ala Thr Asp  
85 90 95

Glu Trp Phe Leu Leu Ser Ser His Ile Pro Leu  
100 105

<210> 16

<211> 116

<212> PRT

<213> Rattus norvegicus

<400> 16

Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val Leu Gln Ala  
1 5 10 15

Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr Val  
20 25 30

Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Tyr Glu Thr Lys Val  
35 40 45

His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe Thr Phe Lys  
50 55 60

Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met Ala Ile Tyr  
65 70 75 80



Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Val Lys Val  
                             85                            90                            95

Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu Trp Arg Asp  
                             100                            105                            110

Leu Gln Gly Gly  
                     115

<210> 17  
 <211> 132  
 <212> PRT  
 <213> Bos taurus

<400> 17  
 Leu Tyr Asp Gln Asp Asn Ser Ser Leu Lys Cys Thr Ile Ile Lys Ala  
   1                            5                            10                            15

Lys Gly Leu Lys Pro Met Asp Ser Asn Gly Leu Ala Asp Pro Tyr Val  
                             20                            25                            30

Lys Leu His Leu Leu Pro Gly Ala Ser Lys Ser Asn Lys Leu Arg Thr  
                             35                            40                            45

Lys Thr Leu Arg Asn Thr Arg Asn Pro Ile Trp Asn Glu Thr Leu Val  
                             50                            55                            60

Tyr His Gly Ile Thr Asp Glu Asp Met Gln Arg Lys Thr Leu Arg Ile  
   65                            70                            75                            80

Ser Val Cys Asp Glu Asp Lys Phe Gly His Asn Glu Phe Ile Gly Glu  
                             85                            90                            95

Thr Arg Phe Ser Leu Lys Lys Leu Lys Pro Asn Gln Arg Lys Asn Phe  
                             100                            105                            110

Asn Ile Cys Leu Glu Arg Val Ile Pro Met Lys Arg Ala Gly Thr Thr  
                             115                            120                            125

Gly Ser Ala Arg  
                     130

<210> 18  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide

<400> 18  
 acgcgtcgac cagagagccc cgcaag

<210> 19  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 19  
 gaagatctag gtctatactg ggccac

26

<210> 20  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 peptide

<400> 20  
 Lys Arg Leu Leu Asp Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln  
 1 5 10 15

Gln Thr Arg Val  
 20

<210> 21  
 <211> 1135  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: mammalian  
 SYNGAP-C

<400> 21  
 Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro  
 1 5 10 15

Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile  
 20 25 30

Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu  
 35 40 45

Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala  
 50 55 60

Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn  
 65 70 75 80

Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile  
 85 90 95

Glu	Ala	Arg	Glu	Leu	Pro	Pro	Lys	Lys	Arg	Tyr	Tyr	Cys	Glu	Leu	Cys	100	105	110
Leu	Asp	Asp	Met	Leu	Tyr	Ala	Arg	Thr	Thr	Ser	Lys	Pro	Arg	Ser	Ala	115	120	125
Ser	Gly	Asp	Thr	Val	Phe	Trp	Gly	Glu	His	Phe	Glu	Phe	Asn	Asn	Leu	130	135	140
Pro	Ala	Val	Arg	Ala	Leu	Arg	Leu	His	Leu	Tyr	Arg	Asp	Ser	Asp	Lys	145	150	155
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 <223> Description of Unknown Organism: mammalian  
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SYNGAP-B

&lt;400&gt; 23

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SYNGAP-C

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